

FILE 'HOME' ENTERED AT 15:23:40 ON 28 FEB 2006

=> fil reg

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

0.21

0.21

FILE 'REGISTRY' ENTERED AT 15:23:51 ON 28 FEB 2006

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STRUCTURE FILE UPDATES: 27 FEB 2006 HIGHEST RN 875402-35-0

DICTIONARY FILE UPDATES: 27 FEB 2006 HIGHEST RN 875402-35-0

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH January 6, 2006

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<http://www.cas.org/ONLINE/UG/regprops.html>

=> s caagctcgccgcggtgcctc/sqsn

L1 7 CAAGCTCGCCGCGGTGCCTC/SQSN

=> d 1-7

L1 ANSWER 1 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN

RN 360469-37-0 REGISTRY

ED Entered STN: 04 Oct 2001

CN DNA (human clone NL1-DD18C genome survey sequence) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AJ334593

FS NUCLEIC ACID SEQUENCE

MF Unspecified

CI MAN

SR GenBank

LC STN Files: CA, CAPLUS, GENBANK

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

*** USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE ***

1 REFERENCES IN FILE CA (1907 TO DATE)

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1800EXS

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	DEC 05	CASREACT(R) - Over 10 million reactions available
NEWS	4	DEC 14	2006 MeSH terms loaded in MEDLINE/LMEDLINE
NEWS	5	DEC 14	2006 MeSH terms loaded for MEDLINE file segment of TOXCENTER
NEWS	6	DEC 14	CA/CAPLUS to be enhanced with updated IPC codes
NEWS	7	DEC 21	IPC search and display fields enhanced in CA/CAPLUS with the IPC reform
NEWS	8	DEC 23	New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/USPAT2
NEWS	9	JAN 13	IPC 8 searching in IFIPAT, IFIUIDB, and IFICDB
NEWS	10	JAN 13	New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to INPADOC
NEWS	11	JAN 17	Pre-1988 INPI data added to MARPAT
NEWS	12	JAN 17	IPC 8 in the WPI family of databases including WPIFV
NEWS	13	JAN 30	Saved answer limit increased
NEWS	14	JAN 31	Monthly current-awareness alert (SDI) frequency added to TULSA
NEWS	15	FEB 21	STN AnaVist, Version 1.1, lets you share your STN AnaVist visualization results
NEWS	16	FEB 22	Status of current WO (PCT) information on STN
NEWS	17	FEB 22	The IPC thesaurus added to additional patent databases on STN
NEWS	18	FEB 22	Updates in EPFULL; IPC 8 enhancements added
NEWS	19	FEB 27	New STN AnaVist pricing effective March 1, 2006
NEWS EXPRESS			FEBRUARY 15 CURRENT VERSION FOR WINDOWS IS V8.01a, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005. V8.0 AND V8.01 USERS CAN OBTAIN THE UPGRADE TO V8.01a AT http://download.cas.org/express/v8.0-Discover/
NEWS HOURS			STN Operating Hours Plus Help Desk Availability
NEWS INTER			General Internet Information
NEWS LOGIN			Welcome Banner and News Items
NEWS PHONE			Direct Dial and Telecommunication Network Access to STN
NEWS WWW			CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

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* * * * * STN Columbus * * * * *

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L1 ANSWER 2 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN
RN 360469-33-6 REGISTRY
ED Entered STN: 04 Oct 2001
CN DNA (human clone NL1-CP9C genome survey sequence) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AJ334589
FS NUCLEIC ACID SEQUENCE
MF Unspecified
CI MAN
SR GenBank
LC STN Files: CA, CAPLUS, GENBANK

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1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L1 ANSWER 3 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN
RN 360349-62-8 REGISTRY
ED Entered STN: 04 Oct 2001
CN DNA (human clone NL1-HD1C genome survey sequence) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AJ322622
FS NUCLEIC ACID SEQUENCE
MF Unspecified
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1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L1 ANSWER 4 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN
RN 259722-69-5 REGISTRY
ED Entered STN: 22 Mar 2000
CN GenBank AC026121 (9CI) (CA INDEX NAME)
FS NUCLEIC ACID SEQUENCE
MF Unspecified
CI MAN
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L1 ANSWER 5 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN
RN 259344-58-6 REGISTRY
ED Entered STN: 19 Mar 2000
CN DNA (human clone NL1-DD18C genome survey sequence) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AQ938734
FS NUCLEIC ACID SEQUENCE
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RN 259280-21-2 REGISTRY
ED Entered STN: 19 Mar 2000
CN GenBank AC025423 (9CI) (CA INDEX NAME)
FS NUCLEIC ACID SEQUENCE
MF Unspecified
CI MAN
SR GenBank
LC STN Files: GENBANK

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=> d kwic

L1 ANSWER 1 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN

SEQ 51 gccacacagg cccagaagc agccaagctc gccgcggtgc ctcggtgcgc
=====

HITS AT: 74-93

=> d sql

L1 ANSWER 1 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN
SQL 671

\$%^STN;HighlightOn= ***;HighlightOff=*** ;

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1800EXS

PASSWORD:

* * * * * RECONNECTED TO STN INTERNATIONAL * * * * *

SESSION RESUMED IN FILE 'HOME' AT 14:01:37 ON 28 FEB 2006

FILE 'HOME' ENTERED AT 14:01:37 ON 28 FEB 2006

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

=> fil registry

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'REGISTRY' ENTERED AT 14:02:06 ON 28 FEB 2006

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DICTIONARY FILE UPDATES: 27 FEB 2006 HIGHEST RN 875402-35-0

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L1 7 CAAGCTCGCCGCGGTGCCTC/SQSN

=> d tot

L1 ANSWER 1 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN

RN 360469-37-0 REGISTRY

ED Entered STN: 04 Oct 2001

CN DNA (human clone NL1-DD18C genome survey sequence) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AJ334593

FS NUCLEIC ACID SEQUENCE
MF Unspecified
CI MAN
SR GenBank
LC STN Files: CA, CAPLUS, GENBANK

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1 REFERENCES IN FILE CA (1907 TO DATE)
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FS NUCLEIC ACID SEQUENCE
MF Unspecified
CI MAN
SR GenBank
LC STN Files: GENBANK

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*** USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE ***

=> save temp l1 10608463/a
10608463/A IS NOT A VALID SAVED NAME
Enter the name you wish to use for the saved query,
answer set, or L-number list. The name must:
1. Begin with a letter,
2. Have 1-12 characters,
3. Contain only letters (A-Z) and numbers (0-9),
4. End with /Q for a query (search profile,
structure, or screen set), /A for an answer
set, or /L for an L-number list.
5. Not already be in use as a saved name,
6. Not be END, SAV, SAVE, SAVED
7. Not have the form of an L-number (Lnnn).
ENTER NAME OR (END):end

=> log h
COST IN U.S. DOLLARS
FULL ESTIMATED COST

	SINCE FILE	TOTAL
	ENTRY	SESSION
	47.03	47.24

SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 14:09:13 ON 28 FEB 2006

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1800EXS

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

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NEWS HOURS STN Operating Hours Plus Help Desk Availability
NEWS INTER General Internet Information
NEWS LOGIN Welcome Banner and News Items
NEWS PHONE Direct Dial and Telecommunication Network Access to STN
NEWS WWW CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 15:23:40 ON 28 FEB 2006

=> fil reg

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.21

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L1      7 CAAGCTCGCCGCGGTGCCTC/SQSN
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=> d 1-7
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=> d kwic

L1 ANSWER 1 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN

SEQ 51 gccacacagg cccagaagc agccaagctc gccgcggtgc ctcggtgcgc
=====

HITS AT: 74-93

=> d sql

L1 ANSWER 1 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN
SQL 671

=> d 4-7 kwic sql

L1 ANSWER 4 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN

SEQ 138251 gggccacaca ggccccagaa gcagccaagc tcgccgcggt gcctcggtgc
=====

HITS AT: 138276-138295

SQL 144450

L1 ANSWER 5 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN

SEQ 51 gccacacagg ccccagaagc agccaagctc gccgcggtgc ctcggtgcgc
=====

HITS AT: 74-93

SQL 647

L1 ANSWER 6 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN

SEQ 51 gccacacagg ccccataagc agccaagctc gccgcggtgc ctctgtgcgc
=====

HITS AT: 74-93

SQL 456

L1 ANSWER 7 OF 7 REGISTRY COPYRIGHT 2006 ACS on STN


SEQ 141251 acacaggccc cagaagcagc caagctcgcc gcggtgcctc ggtgcgcgcc
=====

HITS AT: 141271-141290

SQL 150579

=>

Connection closed by remote host


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Display Show

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☒ CDD [F](#)

☐ 1: [AQ938734](#). Reports NL1-DD18C Human N...[gi:7215112] [Links](#)

LOCUS AQ938734 647 bp DNA linear GSS 23-AUG-2000

DEFINITION NL1-DD18C Human NotI clones Homo sapiens genomic, genomic survey sequence.

ACCESSION AQ938734

VERSION AQ938734.1 GI:7215112

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 647)

AUTHORS Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V., Xie,L., Muravenko,O.V., Kozyrev,S., Petrenko,L., Skobeleva,N., Li,J., Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.

TITLE NotI clones in the analysis of the human genome

JOURNAL Nucleic Acids Res. 28 (7), 1635-1639 (2000)

PUBMED 10710430

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Fax: +46-8-337983
Email: Raf.Podowski@cgr.ki.se
Class: NotI site.

FEATURES Location/Qualifiers

source 1..647
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human NotI clones"

ORIGIN

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1  gcggccgccc ctcgggctcg gcttcttctt ccatctttcc gacacacagg gccacacagg
61  ccccagaagc agccaagctc gccgcggtgc ctcggtgcgc gcccctacc gcccgagggg
121 agcgcgcggg tcgtcgcggc gcatccgggc atttgtgcgc gcgcacacaa cgggcccgc
181 ttncgccaat tgggtccggg gctcgccgc accacctcg ggatgatgga gtggggggtt
241 gtncccccgc gggcgcnngt gggctntnag gcggggtggg ggtgttgnc cgtgagctga
301 taggggttgg gctnngcctg gctccggagc caagtanggt ttggcgctgt gacactcctt
361 tagcccggtg cgctatgttt ggattttttg tgtttacact tccnccccgc tgttggaaac
421 ttgcgacaaa tgcnggaatn ttctgtttgc ttggtaccaa aaaagaaacc aaaaattaaa
481 cagctttttc aatatattta nccccactnc accatcccggt ttggagttgt accccaaatg
541 agttttatgt aaggcctgtt ttaaaaaaag aattaaaaat agcactttta ggcagggtt
601 atacaccggg tgcatacaac ttgtttctcg ttgggagaac gaaaaaat

```

//



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

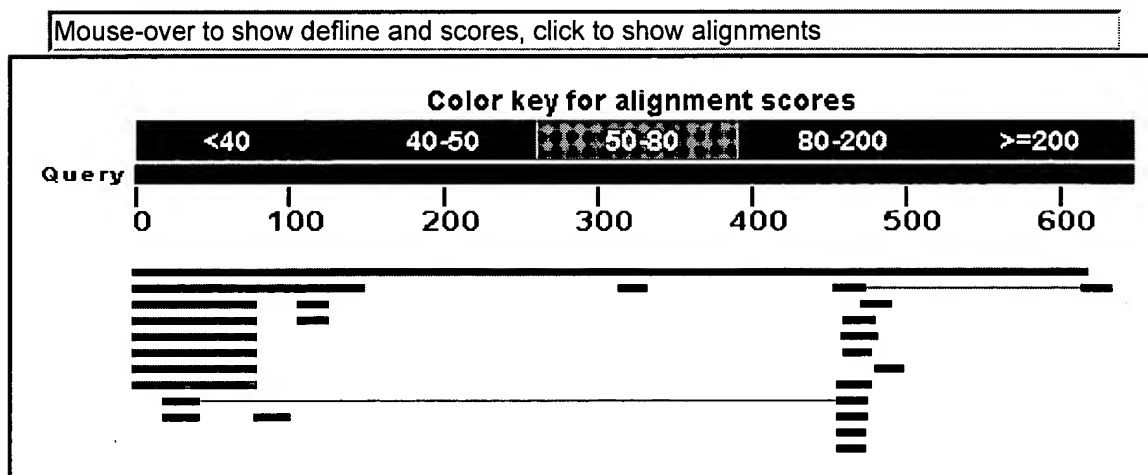
RID: 1141159146-24203-35334814506.BLASTQ1

Database: NCBI Genomic Reference Sequences
636,618 sequences; 5,837,283,223 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=647

Distribution of 28 Blast Hits on the Query Sequence



Sequences producing significant alignments:			Score (Bits)	E Value
gi 51511728 ref NC_000012.9 NC_000012	Homo sapiens chromosome 12		<u>611</u>	4e-172
gi 55638476 ref XM_509211.1 	PREDICTED: Pan troglodytes simil...		<u>293</u>	1e-76
gi 46488912 ref NM_006881.2 	Homo sapiens Mdm2, transformed 3...		<u>161</u>	1e-36
gi 46488906 ref NM_006882.2 	Homo sapiens Mdm2, transformed 3...		<u>161</u>	1e-36
gi 46488903 ref NM_002392.2 	Homo sapiens Mdm2, transformed 3...		<u>161</u>	1e-36
gi 46488904 ref NM_006878.2 	Homo sapiens Mdm2, transformed 3...		<u>161</u>	1e-36

gi 46488908 ref NM_006879.2	Homo sapiens Mdm2, transformed 3...	161	1e-36
gi 46488910 ref NM_006880.2	Homo sapiens Mdm2, transformed 3...	161	1e-36
gi 51511461 ref NC_000001.8 NC_000001	Homo sapiens chromosome 1,	44.1	0.19
gi 72185816 ref NC_003282.3	Caenorhabditis elegans chromosome I	42.1	0.76
gi 78042616 ref NC_007503.1	Carboxydotherrhus hydrogenoformans Z	42.1	0.76
gi 30698031 ref NC_003071.3	Arabidopsis thaliana chromosome 2,	42.1	0.76
gi 86562519 ref NC_003280.4	Caenorhabditis elegans chromosome I	40.1	3.0
gi 86561680 ref NC_003279.4	Caenorhabditis elegans chromosome I	40.1	3.0
gi 50953925 ref NC_006087.1	Leifsonia xyli subsp. xyli str. CTC	40.1	3.0
gi 55613958 ref XM_515905.1	PREDICTED: Pan troglodytes simil...	40.1	3.0
gi 71992358 ref NM_062300.4	Caenorhabditis elegans Signal El...	40.1	3.0
gi 67473823 ref XM_647569.1	Entamoeba histolytica HM-1:IMSS ...	40.1	3.0
gi 66508964 ref XM_624823.1	PREDICTED: Apis mellifera simila...	40.1	3.0
gi 42406306 ref NC_000019.8 NC_000019	Homo sapiens chromosome 19	40.1	3.0
gi 51511730 ref NC_000014.7 NC_000014	Homo sapiens chromosome 14	40.1	3.0
gi 51511729 ref NC_000013.9 NC_000013	Homo sapiens chromosome 13	40.1	3.0
gi 51511723 ref NC_000007.11 NC_000007	Homo sapiens chromosome 7	40.1	3.0
gi 51511462 ref NC_000002.9 NC_000002	Homo sapiens chromosome 2,	40.1	3.0

Alignments

Get selected sequences

Select all

Deselect all

> ☐ gi|51511728|ref|NC_000012.9|NC_000012 ☒ Homo sapiens chromosome 12, complete sec
Length=132449811

Score = 611 bits (308), Expect = 4e-172
Identities = 563/618 (91%), Gaps = 25/618 (4%)
Strand=Plus/Minus

Query	1	GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG	60
Sbjct	67488327	GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG	67488
Query	61	CCCCAGAAGCAGCCAAGCTCGCCGCGGTGCCTCGGTGCGCGCCCCCTACCGCCCGAGGGG	120
Sbjct	67488267	CCCCAGAAGCAGCCAAGCTCGCCGCGGTGCCTCGGTGCGCGCCCCCTACCGCCCGAGGGG	67488
Query	121	AGCGCGCGGGTCGTCGCGGCGCATCCGGGCATTTGTGCGCGCGCACACAACCGGCCCCGC	180
Sbjct	67488207	AGCGCGCGGGTCGTCGCGGCGCATCCGGGCATTTGTGCGCGCGCACACAACCGGCCCCGC	67488
Query	181	TTNCGCCAATTGGGTCCGGGGCTCGGCCGCACCACCTCCGGGATGATGGAGTGGGGGGTT	240
Sbjct	67488147	TTCCGCCAATTGGGTCCGGGGCTCGGCCGCACCACCTCCGGGATGATGGAGTGGGGGG-T	67488
Query	241	GTCNCCCCGCGGGCGCNGGTGGGCTNTNAGGCGGGGTGGGGGTGTTGNCCCGTGAGCTGA	300
Sbjct	67488088	GTCGCCCCGCGGGCGC-GGCGGGCTGTGAGGCGGGGTGGGGGTGTTGG-CCGCGAGCTGA	67488
Query	301	TAGGGTTGGGGCTNGGCCTGGCTCCGGAGCCAAGTANGGTTTGGCGCTGTGACACTCCTT	360
Sbjct	67488030	GAGGG-TGGGGCTCGGCCTGGC-GCGGAGCC-AGCAAGGTTTGGCGCTGTGACACTCCTT	67487
Query	361	TAGCCCGGTGCGCTATGTTTGGATTTTTTGTGTTTACACTTCCNCCCCTGTTGGAAAC	420

Score = 42.1 bits (21), Expect = 0.76
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Minus

Score = 42.1 bits (21), Expect = 0.76
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Minus

Score = 293 bits (148), Expect = 1e-76
Identities = 151/152 (99%), Gaps = 0/152 (0%)
Strand=Plus/Minus

2/28/06

> [gi|46488912|ref|NM_006881.2|](#) **U|E|G** Homo sapiens Mdm2, transformed 3T3 cell doub:
binding protein (mouse) (MDM2), transcript variant MDM2d, mRNA
Length=1540

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus

```
Query 1 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
      |||
Sbjct 81 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61 CCCCAGAAGCAGCCAAGCTCG 81
      |||
Sbjct 21 CCCCAGAAGCAGCCAAGCTCG 1
```

> [gi|46488906|ref|NM_006882.2|](#) **U|E|G** Homo sapiens Mdm2, transformed 3T3 cell doub:
binding protein (mouse) (MDM2), transcript variant MDM2e, mRNA
Length=1403

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus

```
Query 1 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
      |||
Sbjct 81 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61 CCCCAGAAGCAGCCAAGCTCG 81
      |||
Sbjct 21 CCCCAGAAGCAGCCAAGCTCG 1
```

> [gi|46488903|ref|NM_002392.2|](#) **U|E|G** Homo sapiens Mdm2, transformed 3T3 cell doub:
binding protein (mouse) (MDM2), transcript variant MDM2, mRNA
Length=2357

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus

```
Query 1 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
      |||
Sbjct 81 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61 CCCCAGAAGCAGCCAAGCTCG 81
      |||
Sbjct 21 CCCCAGAAGCAGCCAAGCTCG 1
```

> [gi|46488904|ref|NM_006878.2|](#) **U|E|G** Homo sapiens Mdm2, transformed 3T3 cell doub:
binding protein (mouse) (MDM2), transcript variant MDM2a, mRNA
Length=1613

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus


```

Query 1  GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
        |||
Sbjct 81  GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61  CCCCAGAAGCAGCCAAGCTCG 81
        |||
Sbjct 21  CCCCAGAAGCAGCCAAGCTCG 1

```

> [gi|46488908|ref|NM_006879.2|](#) **U|G** Homo sapiens Mdm2, transformed 3T3 cell double binding protein (mouse) (MDM2), transcript variant MDM2b, mRNA
Length=1143

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus

```

Query 1  GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
        |||
Sbjct 81  GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61  CCCCAGAAGCAGCCAAGCTCG 81
        |||
Sbjct 21  CCCCAGAAGCAGCCAAGCTCG 1

```

> [gi|46488910|ref|NM_006880.2|](#) **U|E|G** Homo sapiens Mdm2, transformed 3T3 cell double binding protein (mouse) (MDM2), transcript variant MDM2c, mRNA
Length=1490

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus

```

Query 1  GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
        |||
Sbjct 81  GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61  CCCCAGAAGCAGCCAAGCTCG 81
        |||
Sbjct 21  CCCCAGAAGCAGCCAAGCTCG 1

```

> [gi|51511461|ref|NC_000001.8|NC_000001](#) **D** Homo sapiens chromosome 1, complete sequence
Length=245522847

Score = 44.1 bits (22), Expect = 0.19
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```

Query 454      GTACCAAAAAAGAAACCAAAAA 475
        |||
Sbjct 226665019 GTACCAAAAAAGAAACCAAAAA 226664998

```

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 615 TACAACCTGTTTCTGGTTGG 634
 |||||
 Sbjct 182980638 TACAACCTGTTTCTGGTTGG 182980619

> [gi|72185816|ref|NC_003282.3|](#) **D** *Caenorhabditis elegans* chromosome IV, complete se
 Length=17493785

Features in this part of subject sequence:
Y54G2A.11a

Score = 42.1 bits (21), Expect = 0.76
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query 472 AAAATTAAACAGCTTTTTC AA 492
 |||||
 Sbjct 2769893 AAAATTAAACAGCTTTTTC AA 2769913

> [gi|78042616|ref|NC_007503.1|](#) **D** *Carboxydotherrmus hydrogenoformans* Z-2901, complet
 Length=2401520

Features flanking this part of subject sequence:
18 bp at 5' side: stage II sporulation protein R
57 bp at 3' side: sporulation sigma factor SigG

Score = 42.1 bits (21), Expect = 0.76
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query 461 AAAAGAAACCAAAAATTAAAC 481
 |||||
 Sbjct 1840215 AAAAGAAACCAAAAATTAAAC 1840235

> [gi|30698031|ref|NC_003071.3|](#) **D** *Arabidopsis thaliana* chromosome 2, complete sequ
 Length=19705359

Features flanking this part of subject sequence:
806 bp at 5' side: unknown protein
3563 bp at 3' side: hydrolase

Score = 42.1 bits (21), Expect = 0.76
 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Minus

Query 459 AAAAAAGAAACCAAAAATTAAACAG 483
 |||||
 Sbjct 293325 AAAAAAGAAAGCAAAAATTAAACAG 293301

> [gi|86562519|ref|NC_003280.4|](#) **D** *Caenorhabditis elegans* chromosome II, complete se
 Length=15279313

Features in this part of subject sequence:
Signal Element on Autosome family member (sea-2)

Score = 40.1 bits (20), Expect = 3.0

Identities = 23/24 (95%), Gaps = 0/24 (0%)
Strand=Plus/Minus

```
Query 21      GCTTCTTGCTCCATCTTTCCGACA 44
              |||
Sbjct 3967543 GCTTCTTGCTCCATCTTGCCGACA 3967520
```

Features flanking this part of subject sequence:

2854 bp at 5' side: C01G12.8

423 bp at 3' side: Trehalose 6-Phosphate Synthase family member (tps-2)

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

```
Query 457      CCAAAAAAGAAACCAAAAAT 476
              |||
Sbjct 14600379 CCAAAAAAGAAACCAAAAAT 14600360
```

> [gi|86561680|ref|NC_003279.4|](#) **D** *Caenorhabditis elegans* chromosome I, complete sequence
Length=15072418

Features in this part of subject sequence:

F56G4.6

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query 460      AAAAAGAAACCAAAAATTAA 479
              |||
Sbjct 11369416 AAAAAGAAACCAAAAATTAA 11369435
```

> [gi|50953925|ref|NC_006087.1|](#) **D** *Leifsonia xyli* subsp. *xyli* str. CTCB07, complete sequence
Length=2584158

Features in this part of subject sequence:

two-component system, response regulator

Score = 40.1 bits (20), Expect = 3.0
Identities = 23/24 (95%), Gaps = 0/24 (0%)
Strand=Plus/Minus

```
Query 80      CGCCGCGGTGCCTCGGTGCGCGCC 103
              |||
Sbjct 74069   CGCCGCGGTGTCTCGGTGCGCGCC 74046
```

> [gi|55613958|ref|XM_515905.1|](#) **G** PREDICTED: *Pan troglodytes* similar to methionine 1D; similar to methionine aminopeptidase-like 1; CDS of metAP-3 within PCR fragment (LOC459738), mRNA
Length=969

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

```
Query 109 CCGCCCGAGGGGAGCGCGCG 128
          |||
Sbjct 212 CCGCCCGAGGGGAGCGCGCG 193
```

> [gi|71992358|ref|NM_062300.4|](#) **G** *Caenorhabditis elegans* Signal Element on Autosome (sea-2) (sea-2) mRNA, complete cds
Length=5867

Score = 40.1 bits (20), Expect = 3.0
Identities = 23/24 (95%), Gaps = 0/24 (0%)
Strand=Plus/Minus

```
Query 21 GCTTCTTGCTCCATCTTTCCGACA 44
          |||
Sbjct 3266 GCTTCTTGCTCCATCTTGCCGACA 3243
```

> [gi|67473823|ref|XM_647569.1|](#) **G** *Entamoeba histolytica* HM-1:IMSS hypothetical prot mRNA, partial cds
Length=1002

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

```
Query 481 CAGCTTTTTCAATATATTTA 500
          |||
Sbjct 259 CAGCTTTTTCAATATATTTA 240
```

> [gi|66508964|ref|XM_624823.1|](#) **G** PREDICTED: *Apis mellifera* similar to ENSANGP00000 mRNA
Length=1128

Score = 40.1 bits (20), Expect = 3.0
Identities = 23/24 (95%), Gaps = 0/24 (0%)
Strand=Plus/Plus

```
Query 456 ACCAAAAAAGAAACCAAAAATTAA 479
          |||
Sbjct 918 ACCAGAAAAGAAACCAAAAATTAA 941
```

> [gi|42406306|ref|NC_000019.8|NC_000019](#) **D** *Homo sapiens* chromosome 19, complete sec
Length=63811651

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query 315 GGCCTGGCTCCGGAGCCAAG 334
          |||
Sbjct 34762938 GGCCTGGCTCCGGAGCCAAG 34762957
```

> [gi|51511730|ref|NC_000014.7|NC_000014](#) **D** *Homo sapiens* chromosome 14, complete sec

Length=106368585

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 457 CCAAAAAAGAAACCAAAAT 476
|||||
Sbjct 53001238 CCAAAAAAGAAACCAAAAT 53001219

> [gi|51511729|ref|NC_000013.9|NC_000013](#) **D** Homo sapiens chromosome 13, complete seq
Length=114142980

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 456 ACCAAAAAGAAACCAAAA 475
|||||
Sbjct 71530807 ACCAAAAAGAAACCAAAA 71530788

> [gi|51511723|ref|NC_000007.11|NC_000007](#) **D** Homo sapiens chromosome 7, complete seq
Length=158628139

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 456 ACCAAAAAGAAACCAAAA 475
|||||
Sbjct 3586270 ACCAAAAAGAAACCAAAA 3586251

> [gi|51511462|ref|NC_000002.9|NC_000002](#) **D** Homo sapiens chromosome 2, complete seq
Length=243018229

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 109 CCGCCCGAGGGGAGCGCGCG 128
|||||
Sbjct 172690288 CCGCCCGAGGGGAGCGCGCG 172690269

Get selected sequences

Select all

Deselect all

Database: NCBI Genomic Reference Sequences

Posted date: Feb 7, 2006 12:38 PM

Number of letters in database: 1,542,315,927

Number of sequences in database: 636,618

Lambda K H
1.37 0.711 1.31
Gapped

Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 636618
Number of Hits to DB: 12299377
Number of extensions: 672028
Number of successful extensions: 11473
Number of sequences better than 10: 5
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 11468
Number of HSP's successfully gapped: 10
Length of query: 647
Length of database: 5837283223
Length adjustment: 21
Effective length of query: 626
Effective length of database: 5837283223
Effective search space: 3654139297598
Effective search space used: 3645770317370
A: 0
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 14 (28.2 bits)
S2: 20 (40.1 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

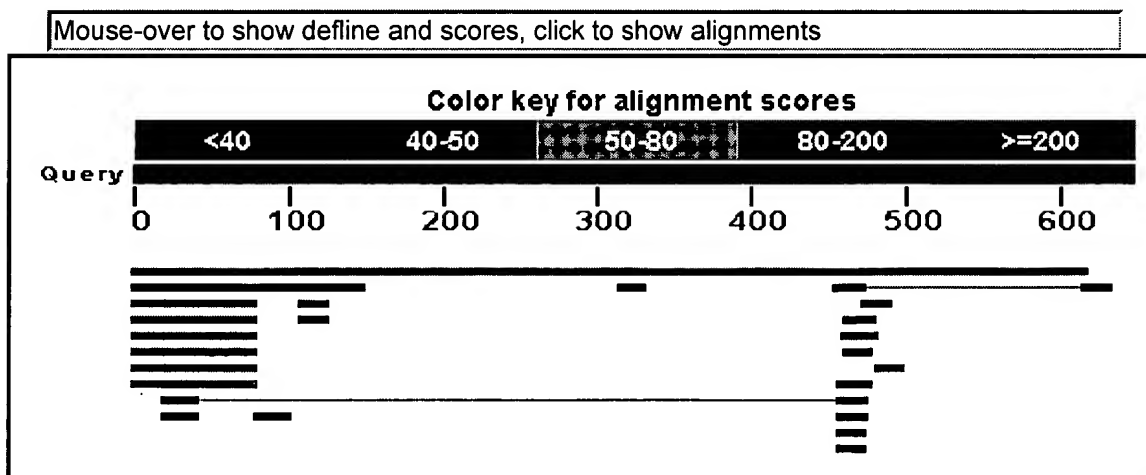
RID: 1141159146-24203-35334814506.BLASTQ1

Database: NCBI Genomic Reference Sequences
636,618 sequences; 5,837,283,223 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=647

Distribution of 28 Blast Hits on the Query Sequence



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gi 46488906 ref NM_006882.2	Homo sapiens Mdm2, transformed 3...		161	1e-36
gi 46488903 ref NM_002392.2	Homo sapiens Mdm2, transformed 3...		161	1e-36
gi 46488904 ref NM_006878.2	Homo sapiens Mdm2, transformed 3...		161	1e-36

gi 46488908 ref NM_006879.2	Homo sapiens Mdm2, transformed 3...	161	1e-36
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gi 51511461 ref NC_000001.8 NC_000001	Homo sapiens chromosome 1,	44.1	0.19
gi 72185816 ref NC_003282.3	Caenorhabditis elegans chromosome I	42.1	0.76
gi 78042616 ref NC_007503.1	Carboxydotherrhus hydrogeniformans Z	42.1	0.76
gi 30698031 ref NC_003071.3	Arabidopsis thaliana chromosome 2,	42.1	0.76
gi 86562519 ref NC_003280.4	Caenorhabditis elegans chromosome I	40.1	3.0
gi 86561680 ref NC_003279.4	Caenorhabditis elegans chromosome I	40.1	3.0
gi 50953925 ref NC_006087.1	Leifsonia xyli subsp. xyli str. CTC	40.1	3.0
gi 55613958 ref XM_515905.1	PREDICTED: Pan troglodytes simil...	40.1	3.0
gi 71992358 ref NM_062300.4	Caenorhabditis elegans Signal El...	40.1	3.0
gi 67473823 ref XM_647569.1	Entamoeba histolytica HM-1:IMSS ...	40.1	3.0
gi 66508964 ref XM_624823.1	PREDICTED: Apis mellifera simila...	40.1	3.0
gi 42406306 ref NC_000019.8 NC_000019	Homo sapiens chromosome 19	40.1	3.0
gi 51511730 ref NC_000014.7 NC_000014	Homo sapiens chromosome 14	40.1	3.0
gi 51511729 ref NC_000013.9 NC_000013	Homo sapiens chromosome 13	40.1	3.0
gi 51511723 ref NC_000007.11 NC_000007	Homo sapiens chromosome 7	40.1	3.0
gi 51511462 ref NC_000002.9 NC_000002	Homo sapiens chromosome 2,	40.1	3.0

Alignments

Get selected sequences

Select all

Deselect all

> ☐ gi|51511728|ref|NC_000012.9|NC_000012 **D** Homo sapiens chromosome 12, complete sec
Length=132449811

Score = 611 bits (308), Expect = 4e-172
Identities = 563/618 (91%), Gaps = 25/618 (4%)
Strand=Plus/Minus

```

Query 1      GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
             |||
Sbjct 67488327 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 67488

Query 61     CCCCAGAAGCAGCCAAGCTCGCCGCGGTGCCTCGGTGCGCGCCCCCTACCGCCCGAGGGG 120
             |||
Sbjct 67488267 CCCCAGAAGCAGCCAAGCTCGCCGCGGTGCCTCGGTGCGCGCCCCCTACCGCCCGAGGGG 67488

Query 121    AGCGCGCGGGTCGTGCGGGCGCATCCGGGCATTTGTGCGCGCGCACACAACCGGCCCCGC 180
             |||
Sbjct 67488207 AGCGCGCGGGTCGTGCGGGCGCATCCGGGCATTTGTGCGCGCGCACACAACCGGCCCCGC 67488

Query 181    TTNCGCCAATTGGGTCCGGGGCTCGGCCGCACCACCTCCGGGATGATGGAGTGGGGGGTT 240
             ||
Sbjct 67488147 TTCCGCCAATTGGGTCCGGGGCTCGGCCGCACCACCTCCGGGATGATGGAGTGGGGGG-T 67488

Query 241    GTCNCCCCGCGGGGCGCNGGTGGGCTNTNAGGCGGGGTGGGGGTGTTGNCCCGTGAGCTGA 300
             |||
Sbjct 67488088 GTCGCCCCGCGGGGCGC-GGCGGGCTGTGAGGCGGGGTGGGGGTGTTGG-CCGCGAGCTGA 67488

Query 301    TAGGGTTGGGGCTNGGCCTGGCTCCGGAGCCAAGTANGGTTTGGCGCTGTGACACTCCTT 360
             |||
Sbjct 67488030 GAGGG-TGGGGCTCGGCCTGGC-GCGGAGCC-AGCAAGGTTTGGCGCTGTGACACTCCTT 67487

Query 361    TAGCCCGGTGCGCTATGTTTGGATTTTTTGTGTTTACACTTCCNCCCGCTGTTGGAAAC 420

```



Sbjct	67487973	TAG-CCGTTGCGCTATGTTTGTATTTCCTTGTTTACACTTCCC GCCCGC-GGTGGAAAC	67487
Query	421	TTGCGACAAATGCNGGAATNTTCGTGTTGCTTGGTACCAAAAAAGAAACC AAAAATTAAA	480
Sbjct	67487915	-TGCGACAAATGCGG--ATCTCCGTGTCGC-TGTTACC-AAAAAGAAACC AAAA--TTAA	67487
Query	481	CAGCTTTTTCAATATATTTANCCCCACTNCACCATCCCGGTTGGAGTTGTACCCCAAATG	540
Sbjct	67487862	CAGCTGTTT-AATATA-TTAAGCCCACTCCACCAGCC--GCTGGAGTTGTA-CCCAAATG	67487
Query	541	AGTTTATTTTAAGGCCTGTTTTnnnnnnnGAATTAAAAATAGCACTTTAAGGCAGGGCTT	600
Sbjct	67487807	AG-TTATTTTAAGGCCTGTTTTTAAAAAG-ATTAAAAATAGCAC-TTAAGGCA-GGCTT	67487
Query	601	ATACACCGGGTGCATACA	618
Sbjct	67487751	ATACACC-GGTGCATACA	67487735

Score = 42.1 bits (21), Expect = 0.76
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Minus

Query	455	TACCAAAAAAGAAACCAAAAA	475
Sbjct	19304021	TACCAAAAAAGAAACCAAAAA	19304001

Score = 42.1 bits (21), Expect = 0.76
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Minus

Query	455	TACCAAAAAAGAAACCAAAAA	475
Sbjct	100709262	TACCAAAAAAGAAACCAAAAA	100709242

> [gi|55638476|ref|XM_509211.1|](#)  PREDICTED: Pan troglodytes similar to double min
MDM2 (LOC452066), mRNA
Length=1389

Score = 293 bits (148), Expect = 1e-76
Identities = 151/152 (99%), Gaps = 0/152 (0%)
Strand=Plus/Minus

Query	1	GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTCCGACACACAGGGCCACACAGG	60
Sbjct	152	GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTCCGACACACAGGGCCACACAGG	93
Query	61	CCCCAGAAGCAGCCAAGCTCGCCGCGGTGCCTCGGTGCGCGCCCCCTACCGCCCGAGGGG	120
Sbjct	92	CCCCAGAAGCAGCCAAGCTCGCCGCGGTGCCTCGGTGCGCGCCCCCTACCGCCCGAGGGG	33
Query	121	AGCGCGCGGGTTCGTCGCGGCGCATCCGGGCAT	152
Sbjct	32	AGCGCGCGGGTTCGTCGCGGCGCATCCGGGCAT	1

> [gi|46488912|ref|NM_006881.2|](#) **U|E|G** Homo sapiens Mdm2, transformed 3T3 cell doub:
binding protein (mouse) (MDM2), transcript variant MDM2d, mRNA
Length=1540

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus

```
Query 1 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
      |||
Sbjct 81 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61 CCCCAGAAGCAGCCAAGCTCG 81
      |||
Sbjct 21 CCCCAGAAGCAGCCAAGCTCG 1
```

> [gi|46488906|ref|NM_006882.2|](#) **U|E|G** Homo sapiens Mdm2, transformed 3T3 cell doub:
binding protein (mouse) (MDM2), transcript variant MDM2e, mRNA
Length=1403

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus

```
Query 1 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
      |||
Sbjct 81 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61 CCCCAGAAGCAGCCAAGCTCG 81
      |||
Sbjct 21 CCCCAGAAGCAGCCAAGCTCG 1
```

> [gi|46488903|ref|NM_002392.2|](#) **U|E|G** Homo sapiens Mdm2, transformed 3T3 cell doub:
binding protein (mouse) (MDM2), transcript variant MDM2, mRNA
Length=2357

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus

```
Query 1 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
      |||
Sbjct 81 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61 CCCCAGAAGCAGCCAAGCTCG 81
      |||
Sbjct 21 CCCCAGAAGCAGCCAAGCTCG 1
```

> [gi|46488904|ref|NM_006878.2|](#) **U|E|G** Homo sapiens Mdm2, transformed 3T3 cell doub:
binding protein (mouse) (MDM2), transcript variant MDM2a, mRNA
Length=1613

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus

```
Query 1 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
        |||
Sbjct 81 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61 CCCCAGAAGCAGCCAAGCTCG 81
        |||
Sbjct 21 CCCCAGAAGCAGCCAAGCTCG 1
```

> [gi|46488908|ref|NM_006879.2|](#) **U|G** Homo sapiens Mdm2, transformed 3T3 cell double binding protein (mouse) (MDM2), transcript variant MDM2b, mRNA
Length=1143

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus

```
Query 1 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
        |||
Sbjct 81 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61 CCCCAGAAGCAGCCAAGCTCG 81
        |||
Sbjct 21 CCCCAGAAGCAGCCAAGCTCG 1
```

> [gi|46488910|ref|NM_006880.2|](#) **U|E|G** Homo sapiens Mdm2, transformed 3T3 cell double binding protein (mouse) (MDM2), transcript variant MDM2c, mRNA
Length=1490

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%), Gaps = 0/81 (0%)
Strand=Plus/Minus

```
Query 1 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 60
        |||
Sbjct 81 GCGGCCGCCCTCGGGCTCGGCTTCTTGCTCCATCTTTCCGACACACAGGGCCACACAGG 22

Query 61 CCCCAGAAGCAGCCAAGCTCG 81
        |||
Sbjct 21 CCCCAGAAGCAGCCAAGCTCG 1
```

> [gi|51511461|ref|NC_000001.8|NC_000001](#) **D** Homo sapiens chromosome 1, complete sequence
Length=245522847

Score = 44.1 bits (22), Expect = 0.19
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```
Query 454 GTACCAAAAAAGAAACCAAAAA 475
        |||
Sbjct 226665019 GTACCAAAAAAGAAACCAAAAA 226664998
```

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 615 TACAACCTGTTTCTGGTTGG 634
 |||||
 Sbjct 182980638 TACAACCTGTTTCTGGTTGG 182980619

> [gi|72185816|ref|NC_003282.3|](#) **D** *Caenorhabditis elegans* chromosome IV, complete se
 Length=17493785

Features in this part of subject sequence:
Y54G2A.11a

Score = 42.1 bits (21), Expect = 0.76
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query 472 AAAATTAAACAGCTTTTTCAC 492
 |||||
 Sbjct 2769893 AAAATTAAACAGCTTTTTCAC 2769913

> [gi|78042616|ref|NC_007503.1|](#) **D** *Carboxydotherrmus hydrogenoformans* Z-2901, complet
 Length=2401520

Features flanking this part of subject sequence:
18 bp at 5' side: stage II sporulation protein R
57 bp at 3' side: sporulation sigma factor SigG

Score = 42.1 bits (21), Expect = 0.76
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query 461 AAAAGAAACCAAAATTAAAC 481
 |||||
 Sbjct 1840215 AAAAGAAACCAAAATTAAAC 1840235

> [gi|30698031|ref|NC_003071.3|](#) **D** *Arabidopsis thaliana* chromosome 2, complete sequ
 Length=19705359

Features flanking this part of subject sequence:
806 bp at 5' side: unknown protein
3563 bp at 3' side: hydrolase

Score = 42.1 bits (21), Expect = 0.76
 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Minus

Query 459 AAAAAAGAAACCAAAATTAAACAG 483
 |||||
 Sbjct 293325 AAAAAAGAAAGCAAAATTAAACAG 293301

> [gi|86562519|ref|NC_003280.4|](#) **D** *Caenorhabditis elegans* chromosome II, complete se
 Length=15279313

Features in this part of subject sequence:
Signal Element on Autosome family member (sea-2)

Score = 40.1 bits (20), Expect = 3.0

Identities = 23/24 (95%), Gaps = 0/24 (0%)
Strand=Plus/Minus

```
Query  21      GCTTCTTGCTCCATCTTTCCGACA  44
          |||||
Sbjct  3967543 GCTTCTTGCTCCATCTTGCCGACA  3967520
```

Features flanking this part of subject sequence:

2854 bp at 5' side: C01G12.8

423 bp at 3' side: Trehalose 6-Phosphate Synthase family member (tps-2)

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

```
Query  457      CCAAAAAAGAAACCAAAAAT  476
          |||||
Sbjct  14600379 CCAAAAAAGAAACCAAAAAT  14600360
```

> [gi|86561680|ref|NC_003279.4|](#) **D** *Caenorhabditis elegans* chromosome I, complete sequence
Length=15072418

Features in this part of subject sequence:

F56G4.6

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  460      AAAAAGAAACCAAAAATTAA  479
          |||||
Sbjct  11369416 AAAAAGAAACCAAAAATTAA  11369435
```

> [gi|50953925|ref|NC_006087.1|](#) **D** *Leifsonia xyli* subsp. *xyli* str. CTCB07, complete sequence
Length=2584158

Features in this part of subject sequence:

two-component system, response regulator

Score = 40.1 bits (20), Expect = 3.0
Identities = 23/24 (95%), Gaps = 0/24 (0%)
Strand=Plus/Minus

```
Query  80      CGCCGCGGTGCCTCGGTGCGCGCC  103
          |||||
Sbjct  74069    CGCCGCGGTGTCTCGGTGCGCGCC  74046
```

> [gi|55613958|ref|XM_515905.1|](#) **G** PREDICTED: Pan troglodytes similar to methionine 1D; similar to methionine aminopeptidase-like 1; CDS of metAP-3 within PCR fragment (LOC459738), mRNA
Length=969

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 109 CCGCCCGAGGGGAGCGCGCG 128
 |||||
 Sbjct 212 CCGCCCGAGGGGAGCGCGCG 193

> [gi|71992358|ref|NM_062300.4|](#) **G** Caenorhabditis elegans Signal Element on Autosome
 (sea-2) (sea-2) mRNA, complete cds
 Length=5867

Score = 40.1 bits (20), Expect = 3.0
 Identities = 23/24 (95%), Gaps = 0/24 (0%)
 Strand=Plus/Minus

Query 21 GCTTCTTGCTCCATCTTTCCGACA 44
 |||||
 Sbjct 3266 GCTTCTTGCTCCATCTTGCCGACA 3243

> [gi|67473823|ref|XM_647569.1|](#) **G** Entamoeba histolytica HM-1:IMSS hypothetical prot
 mRNA, partial cds
 Length=1002

Score = 40.1 bits (20), Expect = 3.0
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

Query 481 CAGCTTTTCAATATATTTA 500
 |||||
 Sbjct 259 CAGCTTTTCAATATATTTA 240

> [gi|66508964|ref|XM_624823.1|](#) **G** PREDICTED: Apis mellifera similar to ENSANGP00000
 mRNA
 Length=1128

Score = 40.1 bits (20), Expect = 3.0
 Identities = 23/24 (95%), Gaps = 0/24 (0%)
 Strand=Plus/Plus

Query 456 ACCAAAAAAGAAACCAAAAATTAA 479
 |||||
 Sbjct 918 ACCAGAAAAGAAACCAAAAATTAA 941

> [gi|42406306|ref|NC_000019.8|NC_000019](#) **D** Homo sapiens chromosome 19, complete sec
 Length=63811651

Score = 40.1 bits (20), Expect = 3.0
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Plus

Query 315 GGCCTGGCTCCGAGCCAAG 334
 |||||
 Sbjct 34762938 GGCCTGGCTCCGAGCCAAG 34762957

> [gi|51511730|ref|NC_000014.7|NC_000014](#) **D** Homo sapiens chromosome 14, complete sec

Length=106368585

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 457 CCAAAAAAGAAACCAAAAT 476
|||||
Sbjct 53001238 CCAAAAAAGAAACCAAAAT 53001219

> ☐ [gi|51511729|ref|NC_000013.9|NC_000013](#) **D** Homo sapiens chromosome 13, complete sequence
Length=114142980

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 456 ACCAAAAAGAAACCAAAA 475
|||||
Sbjct 71530807 ACCAAAAAGAAACCAAAA 71530788

> ☐ [gi|51511723|ref|NC_000007.11|NC_000007](#) **D** Homo sapiens chromosome 7, complete sequence
Length=158628139

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 456 ACCAAAAAGAAACCAAAA 475
|||||
Sbjct 3586270 ACCAAAAAGAAACCAAAA 3586251

> ☐ [gi|51511462|ref|NC_000002.9|NC_000002](#) **D** Homo sapiens chromosome 2, complete sequence
Length=243018229

Score = 40.1 bits (20), Expect = 3.0
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 109 CCGCCCGAGGGGAGCGCGCG 128
|||||
Sbjct 172690288 CCGCCCGAGGGGAGCGCGCG 172690269

Database: NCBI Genomic Reference Sequences

Posted date: Feb 7, 2006 12:38 PM

Number of letters in database: 1,542,315,927

Number of sequences in database: 636,618

Lambda K H
1.37 0.711 1.31
Gapped

Lambda K H
 1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 636618
Number of Hits to DB: 12299377
Number of extensions: 672028
Number of successful extensions: 11473
Number of sequences better than 10: 5
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 11468
Number of HSP's successfully gapped: 10
Length of query: 647
Length of database: 5837283223
Length adjustment: 21
Effective length of query: 626
Effective length of database: 5837283223
Effective search space: 3654139297598
Effective search space used: 3645770317370
A: 0
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 14 (28.2 bits)
S2: 20 (40.1 bits)